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01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
VICILIN C72 PRECURSOR (ALPHA-GLOBULIN B).
Gossypium hirsutum (Upland cotton).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
                                                                                                                                                                     Chian C.A., Pyle J.B., Legocki A.B., Dure L. III;
"Developmental biochemistry of cottonseed embryogenesis and germination. XVIII. cDNA and amino acid sequences of the member the storage protein families.";
Plant Mol. Biol. 7:475-489(1986).
-i- FUNCTION: SEED STORAGE PROTEIN.
-i- SUBCELLULAR LOCATION: COTYLEDONARY MEMBRANE-BOUND VACUOLAR
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RESULT 3
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JB1_MAILL

GLB1_MAIZE

GLB1_MAIZE

C P15590;

C P15590;

T 01-APR-1990 (Rel. 14, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

T 15-JUL-1999 (Rel. 38, Last annotation update)

T 27-2011_IN-1 S ALLELE PRECURSOR (GLB1-S) (7S-LIKE).
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SEQUENCE STRAIN=CV. J
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SEQUENCE
                          SEQUENCE FROM N.A.
                                                 Magnoliophyta; Liliopsida;
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PIR; A30838; FWCNAB.
HSSP; P50477; 1CAX.
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storage protein; Signal
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                                                 Embryophyta; Tracheophyta; Poales; Poaceae; Zea.
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Pred. No. 1.5e
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SEQUENCE
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Biochem. Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular characterization of the major maize embryo globulin encoded by the Glb1 gene.";
Plant Physiol. 91:636-643(1989).
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use by non-profit institutions as long as its content
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SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS
CONVICILIN, CONGLYCININ, ETC.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MATURE PROTEIN FROM THE PRIMARY TRANSLATION PRODUCT. POLYMORPHISM: THE THREE MOST COMMONLY OCCURRING GLB1 THE DESIGNATION L., I, AND S FOR LARGE, INTERMEDIATE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: THREE PROTEIN-PROCESSING STEPS OCCUR IN THE FORMATION OF
                                                                                                                                                                YGQAYEVKPEDYRQLQDMDLSVFIANVTQGSMMGPFFNTRSTKVVVVASGEADVEMACPH
FGQ--QREGVIIRASQEQIRELTRDDSE---SRHWHIRRGGESSRGPYNLFNKRPLYSNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            storage protein;
                                                       RQSQGGESERERGKGRRSEEEEESSEEQEEVGQGYHTIRARLSPGTAFVVPAGHPFVAVA
                                                                                                                                        HGQLYEADARSFHDLAEHDVSVSFANITAGSMSAPLYNTRSFKIAYVPNGKGYAEIVCPH
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525ED1D00A062976 CRC64;
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P11827;
01-OCT-1989
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                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 10:8245-8261(1982).

-!- FUNCTION: SEED STORAGE PROTEIN. ACCUMULATES DURING SEED

-EVELOPMENT AND IS HYDROLYZED AFTER GERMINATION TO PROVIDE A

CARBON AND NITROGEN SOURCE FOR THE DEVELOPING SEEDLING.

-!- SUBUNIT: THE ALPHA -, ALPHA -, AND BETA-SUBUNITS ASSOCIATE IN

VARIOUS COMBINATIONS TO FORM TRIMERIC PROTEINS.

-!- SUBCELLULAR LOCATION: COTYLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=83143289; PubMed=6897678; Schuler M.A., Ladin B.F., Pollaco J. "Structural sequences are conserved alpha, alpha' and beta-subunits of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOYBN
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BETA-CONGLYCININ, CG-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1989
01-AUG-1992
                                                                                                                                                                          PROPEP
                                                                                                                                                                                                                                                 PFAM;
                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                      EMBL; M13759; AAB01374.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 340-639 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The glycosylated seed storage proteins vulgaris. Structural homologies of genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                          INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Doyle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=86250867; PubMed=3013879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fabales; Fabaceae; Papilionoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem. 261:9228-9238(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: TO OTHER 7S SEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONVICILIN,
                                                                                                                                                                                                                     storage
                                                                                                                                                                                                                                                                                                                      B24810; B24810.
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                                                                                                                                                                                                                                                                                                                                                  J01290;
                                                                                                                                                                                                                                              PF00546; Seedstore_7s;
                                                                                                                                                                                                                                                                                                 P02853; 2PHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J.J., Schuler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           non-profit institutions as long
                                                                                                                                                                                                                                                                     IPR001113; -
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                                                                                                                                                                                                                     protein;
                                                                                                                                                                                                                                                                                                                                            -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONGLYCININ, ETC.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in B.F., Pollaco J.C., Freyer G., Beachy R.N.; nces are conserved in the genes coding for the beta-subunits of the soybean 7S seed storage
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12, Last sequence update)
23, Last annotation updat
ALPHA' CHAIN PRECURSOR.
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543
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74325
                                                                                                                                                                                                                     Signal;
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                 BETA-CONGLYCININ, ALPHA' CHAIN.
N-LINKED (GLCNAC. .) (POTENTIA
N-LINKED (GLCNAC. .) (POTENTIA
P -> L (IN REF. 2).
M -> V (IN REF. 2).
S -> T (IN REF. 2).
                                                                                                                                                                                                                     2.
; Glycoprotein;
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469BF24C79651E3F
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Local Similarity

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p43238;
p43238;
p43238;
p101-NOV-1995 (Rel. 32, Last sequence update)
yr 01-NOV-1995 (Rel. 32, Last sequence update)
yr 01-NOV-1997 (Rel. 35, Last annotation update)
yr 01-NOV-1997 (Rel. 35, Last annotation update)
yr 01-NOV-1997 (Rel. 35, Last annotation update)
yr 01-NOV-1997 (Rel. 32, Last annotation update)
yr 01-NOV-1995 (Rel. 32, Last sequence up
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MEDLINE=96013631; PubMed=7560062;
Burks A.W., Cockrell G., Stanley J.S., Helm R.M., Bannon
"Recombinant peanut allergen Ara h I expression and IgE k
patients with peanut hypersensitivity.";
J. Clin. Invest. 96:1715-1721(1995).
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                                                                                                                           SEQUENCE FROM N.A. STRAIN=CV. FLORUNN
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Rosidae; eurosids I;
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binding
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RPQSQSQSPSSPEKESP
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                                                                                                                                                                                                                                                              FGKLFEVKPDKKNPQLQDLDMMLTCVEIKEGALMLPHFNSKAMVIVVVNKGTGNLELVAV
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Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         patients with peanut hypersensitivity.";
J. Clin. Invest. 96:1715-1721(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CV. FLORUNNER; MEDLINE=96013631; PubMed=7560062;
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VRKEQQQRGRREQEWEEEEEEDEEEEGSNREVRRYTARLKEGDVFIMPAAHPVAINASSEL
                                           PHLSGRHGGRGGGKRHEEEEDVHYE----QVR---ARLSKREAIVVLAGHPVVFVSSGNE
                                                                                            NEGRLEEVKPDKKNPQLQDLDMMLTCVEIKEGALMLPHENSKAMVIVVVNKGTGNLELVA
                                                                                                                        KYGQAYEVKPEDYR-QLQDMDLSVFIANVTQGSMMGPFFNTRSTKVVVVASGEADVEMAC
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                                                                                                                                                                                                                                         R------EGVIIRASQEQIRELTRDDSESRHWHIRRGGESS--RGPYNLFNKRPLYSN
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dons; core eudicots; Rosidae; eurosids I;
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                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: SEED STORAGE PROTEÍN. ACCUMULATES DURING SEED
DEVELOPMENT AND IS HYDROLYZED AFTER GERNIATION TO PROVIDE A
CARBON AND NITROGEN SOURCE FOR THE DEVELOPING SEEDLING.
-!- SUBUNIT: THE ALPHA -, ALPHA -, AND BETA-SUBUNITS ASSOCIATE IN
VARIOUS COMBINATIONS TO FORM TRIMERIC PROTEINS.
-!- SUBCELLULAR LOCATION: EMBRYO AXIS, AND COTYLEDONARY MEMBRANE-BOUND
VACUOLAR PROTEIN BODIES.
-!- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN,
CONVICILIN, CONGLYCININ, ETC.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycine max (Soybean).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1990 (Rel. 13, Created)
01-APR-1990 (Rel. 14, Last sequence upda
15-DEC-1998 (Rel. 37, Last annotation up
BETA-CONGLYCININ, ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                             PFAM; PF00546; Seedstore_7s; Seed storage protein; Signal;
                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                          PIR; S14681; FWSYBA.
                                                                                                                                                                                                                                                                                                                                                          EMBL; X17698; CAA35691.1;
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                                                                                                                                                                                                                                                                                                                INTERPRO;
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                           WSKYDNQEDPQTECQQCQRRCRQQESGPRQQQYCQRRCKEICEEEEEYNRQRD----PQQQ 125
                                                                                    LLFLLSLFLLSTTVS--LAESEFDRQEYEECKRQCMQLETSGQMRRCVSQCDKRFEEDID
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                                                          LLLLGLVFLASVSVSFGIAYWEKENPKHNKCLQSCNSERDSYRNQACHARC
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                                                                                                                               Similarity
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30.5%;
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Pred.
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--LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

CBEBA30506BBBC57 CRC64;
                                                                                                                                                                                                                                                                              Glycoprotein; Multigene family
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01-JAN-1990 (Rel. 13, Last sequence up
01-AUG-1990 (Rel. 15, Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND PARTIAL S
STRAIN=CV. FELTHAM FIRST;
MEDLINE=88326208; PubMed=3415641;
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Eukaryota; Viridiplantae; E
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                                                                                                                                                                                                                                                                                                         Biochem. J. 251:717-726(1988).
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SWISS-PROT entry is copyright. It is produced through a collaboratic een the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no was
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No. 1.5e-43;
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PLANT CELL 4:1561-1574(1992).

PLANT CELL 4:1561-1574(1992).

PLANT CELLULAR LOCATION: MEMBRANE-ASSOCIATED.

PLANT TISSUE SPECIFICITY: ASSOCIATED WITH THE PLASMA MEMBRANE OF SEVERAL CELL TYPES ENGAGED IN SUCROSE TRANSPORT, INCLUDING THE MESOPHYLL CELLS OF YOUNG SINK LEAVES, THE COMPANION CELLS OF MATURE PHLOEM AND THE CELLS OF DEVELOPING COTYLEDONS.

PLANTINE PHLOEM AND THE CELLS OF DEVELOPING COTYLEDONS.

PLANTINE PHLOEM AND THE CELLS OF DEVELOPING COTYLEDONS.

PLANTINE STAGE: IN THE COTYLEDON, EXPRESSION IS NOT DETECTED UNTIL 10 DAYS AFTER FERTILIZATION. BETWEEN 10-19 DAYS AFTER FERTILIZATION, NO DAYS AFTER FERTILIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINB-93104680; PubMed-1467654;
Grimes H.D., Overvoorde P.J., Ripp K., Franceschi
"A 62-kD sucrose binding protein is expressed and
tissues actively engaged in sucrose transport.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
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Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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HSSP; P50477; 1CAW.
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AALNTQTEKLRGVFGQQREGVIIRASQEQIRELTRDDSESRHWHIRRGGESSRGPYNLFN
                                HIPAGTPLYIVNRDENDKLFLAMLHIPVSVSTPGKFEEFFAPGGRDPESVLSAFSWNVLQ
                                                                 RIPAGTTFYLINRDNNERLHIA--KFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILE
                                                                                                    LLQGIENFRLAILEARAHTFVSPRHFDSEVVFFNIKGRAVLGLVSESETEKITLEPGDMI
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29, Last annotation update)
ROTEIN PRECURSOR (SBP).
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_VCLC_PEA
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"Isolation and expression of a pea vicilin cDNA in the yeast Saccharomyces cerevisiae.";
Biochem. J. 251.857-864(1988).
-!- FUNCTION: SEED STORAGE PROTEIN.
-!- SUBCELLULAR LOCATION: COTYLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN
INTERPRO; IPR001113; -.
PFAM; PF00546; SeedStore_7s; 1.
Seed storage protein; Multigene family;
SIGNAL 1 28
CHAIN 29 459 VICILIN.
                                                                                                            PIR; S00567; S00567.
PIR; S08505; S08505.
HSSP; P50477; 1CAW.
                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                     EMBL; X14076; CAA32239.1; EMBL; Y00722; CAA68708.1;
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MEDLINE=88326226; PubMed=3046604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Higgins T.J.V., Newbigin E.J., Spencer D., "The sequence of a pea vicilin gene and it:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Watson M.D., Lambert N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 27-459 FROM N.A. (CLONE PDUB9).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Embryophyta; Tracheophyta; Spermatophyta; Caracheophyta; Spermatophyta; Spermatophyta;
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01-MAY-1992 (Rel. 22, Last sequence upon 101-NOV-1995 (Rel. 32, Last annotation user a condition of the conditi
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01-MAY-1992
01-MAY-1992
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SEQUENCE
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Fabales; Fabace
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                                                                                                                                                                                                                                                                     processes
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"Soybean beta-conglycinin genes are clustered in several DNA regions
and are regulated by transcriptional and posttranscriptional
                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93005638; PubMed=2562562;
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                 FUNCTION: SEED STORAGE PROTEIN. ACCUMULATES DURING SEED DEVELOPMENT AND IS HYDROLYZED AFTER GERMINATION TO PROVIDE CARBON AND NITROGEN SOURCE FOR THE DEVELOPING SEEDLING. SUBUNIT: THE ALPHA', ALPHA-, AND BETA-SUBUNITS ASSOCIATE VARIOUS COMBINATIONS TO FORM TRIMERIC PROTEINS. SUBCELLULAR LOCATION: EMBRYO AXIS, AND COTYLEDONARY MEMBRA VACUOLAR PROTEIN BODIES.
SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, CONVICILIN, CONGLYCININ, ETC.).
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eudicotyledons; core eudicots; Rosidaa
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Best Local S
Matches 159
                                                                                                                                                                              PEA
                                                                         P02854;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-JAN-1990 (Rel. 13, Last annotation update)
PROVICILIN PRECURSOR (TYPE B) (FRAGMENT)
Pisum sativum (Garden pea)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
SEQUENCE
                                      Eukaryota; Viridiplantae; Embryoph
Magnoliophyta; eudicotyledons; cor
Fabales; Fabaceae; Papilionoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
            SEQUENCE
                                                                                                                                                              VCLB_PEA
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JQ0969; FWSYCB.
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59; Conservative
              FROM
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           N.A.
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37.1%;
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lons; core eudicots; Rosidae; eurosids I;
              PDUB7
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; Glycoprotein;
BY SIMILARITY.
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Best Local Similarity
Matches 147; Conserv
                                                                                                             01-AUG-1988
01-AUG-1988
01-JAN-1990
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NON_TER
SEQUENCE
                                                           Vicia faba (Broad bean).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BODIES.
-!- SIMILARITY: TO OTHER 7S S
STRAIN=CV. MINOR; MEDLINE=88096511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 11:2367-2380(1983).
                         SEQUENCE FROM N.A.
                                                Fabales; Fabaceae;
                                                                                                VICILIN PRECURSOR
                                                                                                                                                 P08438;
                                                                                                                                                           VCL_VICEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The vicilin gene family of pea (Pisum sativum L.): a coding sequence for preprovicilin.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00546; Seedstore_7s; 1.
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(Rel. 08, Last sequence up
(Rel. 13, Last annotation
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>410
222
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 PubMed=3697075
                                                Papilionoideae;
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36.9%;
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Pred. No. 3.:
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CLEAVAGE (POTENTIAL)
N-LINKED (GLCNAC. .
                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
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SEQUENCE
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Nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bassuener R., van Nong H., Jung R., Saalbach G., Muentz K., "The primary structure of the predominating vicilin storage subunit from field bean seeds (Vicia faba L. var. minor cv. Nucleic Acids Res. 15:9609-9609(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seed storage protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weschke W., Baeumleir
"Nucleotide sequence
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SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: COTYLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN
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                FAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAAPRKEVEESFNSQDQSIFFPGPRQ
                                                                                                               KFFEITPKRNPQLQDLNIFVNYVEINEGSLLLPHYNSRAIVIVTVNEGKGDFELVGQRNE
                                                                                                                                                                                                                                                                                                                                                 DNPFVFESNRFQTLFENENGHIRLLQKFDQHSKLLENLQNYRLLEYKSKPHTIFLPQQTD 92
                                                                                   GRHGGRGGGKRHEEEEDVHYEQVR-----ARLSKREAIVVLAGHPVVFVSSGNENLLL
                                                                                                                                         QAYEVKPEDYRQLQDMDLSVFIANVTQGSMMGPFFNTRSTKVVVVASGEADVEMACPHLS
                                                                                                                                                                                                                                                            ISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTEKLRGVFGQ----
                                                                                                                                                                                                                                                                                                                    ADAILLVIGGRGALKMIHHDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAKFLQT 368
-GFGINAENNQRYFLAGEEDNVISQIHKPVKELAFPGSAQEVDTLLENQKQSHFANAQPR
                                                         NQQGLR
                                                                                                                                                                       DRRQRGQEENVIVKISRKQIEELNKNAKSSS----KKSTSSESEPFNLRSREPIYSNKFG
                                                                                                                                                                                                                                 VNRPGEPQSFLLSGNQNQPSILSGFSKNILEASFNTDYKEIEKVLLEEHGKEKYHRRGLK 212
                                                                                                                                                                                                                                                                                         ADFILVVLSGKAILTVLLPNDRNSFSLERGDTIKLPAGTIGYLVNRDDEEDLRVLDLVIP 152
                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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257
443
463
                                                                                                                                                                                         -QREGVIIRASQEQIRELTRDDSESRHWHIRRGGESSRGPYNLFNKRPLYSNKYG
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                                                       EEYDEEKEQGEEEIRKQVQNYKAKLSPGDVLVIPAGYPVAIKASSNLNLV-
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52694 MW;
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257
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                                                                                                                                                                                                                                                                                                                                                                                                          Score 697.5;
Pred. No. 4.8e
39; Mismatches
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4.8e-36;
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                                                                                                                                       Query Match
Best Local
                                                                                                           Matches
                                                                                                                                                                                              PDB; 1CAX; 31.
PDB; 1CAX; 31.
INTERPRO; IPRO01113; -.
PFAM; PFO0546; Seedstore_7s; 1.
PFAM; PFO0546; Seedstore_7s; 1.
Seed storage protein; Signal; 3D-structure.
BY SIMILARITY.
1 26 BY SIMILARITY.
1 26 CANAVALIN.
27 445 CANAVALIN.
27 445 CANAVALIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=COTYLEDON;
MEDLINE=94143475; PubMed=8310055;
Mg J.D., Ko T.-P., McPherson A.;
"Cloning, expression, and crystallization ensiformis) canavalin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Canavalia ensiformis (Jack bean) (Horse bean).

Cukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; eudicotyjedons; core eudicots; Rosidae; eurosids I;

Fabales; Fabaceae; Papilionoideae; Canavalia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ng J.D., Stinchcombe T., Ko T.-P., Alexander E., McPherson A.; "PCR cloning of the full-length cDNA for the seed protein canavalin from the jack bean plant, Canavalis ensiformis."; Plant Mol. Biol. 18:147-149(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CANA_CANEN
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"The three-dimensional structure of canavalin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CANAVALIN PRECURSOR.
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                                                    235 GGSGRYEEGEEEQS----DNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRL 291
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                                                                                                                                          Local Similarity
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GHSGGEAEDESEESRAQNNPYLFRSNKFLTLFKNQHGSLRLLQRFNEDTEKLENLRDYRV
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31-OCT-93.
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                                                                                                                                       674; DB 1;
No. 1.3e-34;
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                                                                                                                                                                    Length 445
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                                               modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
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01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation updat
                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extra the European Bioinformatics Institute. There are no restricted the succession of the succes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamauchi D., Nakamura K., Asahi T., Minamikawa T.;
"CDNAs for canavalin and concanavalin A from Canavalia gladiata
seeds. Nucleotide seguence of cDNA for canavalin and RNA blot
seeds. Nucleotide seguence of cDNA for canavalin and RNA seeds.";
analysis of canavalin and concanavalin A mRNAs in developing seeds.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canavalia gladiata (Sword bean) (Japanese jack bean).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CANAVALIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 17:4381-4381(198-i- FUNCTION: SEED STORAGE PROTEIN.
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Yamauchi D., Nakamura K., Asahi T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eur. J. Biochem. 170:515-520(1988).
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                                                                                                                                                                                                                                                                    SUBUNIT: HOMOTRIMER.
SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, CONVICILIN, CONGLYCININ, ETC.).
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